

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/586,720
Source: JFWP
Date Processed by STIC: 7/31/06

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IFWP

RAW SEQUENCE LISTING DATE: 07/31/2006
 PATENT APPLICATION: US/10/586,720 TIME: 14:43:44

Input Set : A:\NEB-238-PUS.ST25.txt
 Output Set: N:\CRF4\07312006\J586720.raw

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3 <110> APPLICANT: New England Biolabs, Inc.
4      Maina, Claude V.
5      Tzertzinis, George
6      Kumar, Sanjay
8 <120> TITLE OF INVENTION: Compositions and Methods for Generating Short
Double-Stranded RNA
9      Using Mutated RNase III
11 <130> FILE REFERENCE: NEB-238-PUS
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/586,720
C--> 13 <141> CURRENT FILING DATE: 2006-07-20
13 <150> PRIOR APPLICATION NUMBER: PCT/US05/02029
14 <151> PRIOR FILING DATE: 2005-01-21
16 <150> PRIOR APPLICATION NUMBER: 60/538,805
17 <151> PRIOR FILING DATE: 2004-01-23
19 <150> PRIOR APPLICATION NUMBER: 60/572,240
20 <151> PRIOR FILING DATE: 2004-05-18
22 <150> PRIOR APPLICATION NUMBER: 60/543,880
23 <151> PRIOR FILING DATE: 2004-02-12
25 <160> NUMBER OF SEQ ID NOS: 26
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 31
31 <212> TYPE: DNA
32 <213> ORGANISM: unknown
34 <220> FEATURE:
35 <223> OTHER INFORMATION: primer
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43 <212> TYPE: DNA
44 <213> ORGANISM: unknown
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55 <212> TYPE: DNA
56 <213> ORGANISM: unknown
58 <220> FEATURE:
59 <223> OTHER INFORMATION: primer
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62 cagtaaacat aacgcgcgtt tagaat

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Input Set : A:\NEB-238-PUS.ST25.txt
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65 <210> SEQ ID NO: 4
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90 <211> LENGTH: 33
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92 <213> ORGANISM: unknown
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95 <223> OTHER INFORMATION: primer
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102 <211> LENGTH: 20
103 <212> TYPE: DNA
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106 <220> FEATURE:
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110 taatacgact cactataggg 20
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114 <211> LENGTH: 38
115 <212> TYPE: DNA
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118 <220> FEATURE:
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122 taatacgact cactatagaa ggacagatgg ttaagtac 38
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126 <211> LENGTH: 225
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128 <213> ORGANISM: unknown
130 <220> FEATURE:
131 <223> OTHER INFORMATION: relevant region from Pasteurella multocida
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135 Met Thr Gln Asn Leu Glu Arg Leu Gln Arg Gln Ile Gly Tyr Gln Phe
136 1 5 10 15

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139 Asn Gln Pro Ala Leu Leu Lys Gln Ala Leu Thr His Arg Ser Ala Ala
 140 20 25 30
 143 Val Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Ile Leu Asn
 144 35 40 45
 147 Phe Ile Ile Ala Glu Ala Leu Tyr His Gln Phe Pro Lys Cys Asn Glu
 148 50 55 60
 151 Gly Glu Leu Ser Arg Met Arg Ala Thr Leu Val Arg Glu Pro Thr Leu
 152 65 70 75 80
 155 Ala Ser Leu Ala Arg Gln Phe Glu Leu Gly Asp Tyr Leu Ser Leu Gly
 156 85 90 95
 159 Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu Ala
 160 100 105 110
 163 Asp Cys Val Glu Ala Ile Ile Gly Ala Ile Ser Leu Asp Ser Asp Leu
 164 115 120 125
 167 Ala Thr Thr Thr Lys Ile Val Gln His Trp Tyr Gln Ala Gln Leu Lys
 168 130 135 140
 171 Gln Ile Gln Pro Gly Asp Asn Gln Lys Asp Pro Lys Thr Arg Leu Gln
 172 145 150 155 160
 175 Glu Tyr Leu Gln Gly Lys Arg Leu Pro Leu Pro Thr Tyr Asn Val Val
 176 165 170 175
 179 Glu Ile Lys Gly Glu Ala His Cys Gln Thr Phe Thr Val Glu Cys Tyr
 180 180 185 190
 183 Val Lys Asn Ile Asp Arg Thr Phe Met Gly Ser Gly Ala Ser Arg Arg
 184 195 200 205
 187 Lys Ala Glu Gln Ala Ala Ala Glu Lys Ile Leu Gln Leu Leu Glu Met
 188 210 215 220
 191 Lys
 192 225
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 196 <211> LENGTH: 227
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 198 <213> ORGANISM: unknown
 200 <220> FEATURE:
 201 <223> OTHER INFORMATION: relevant region from H. Influenzae
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 206 1 5 10 15
 209 Asp Ile Ala Leu Leu Lys Gln Ala Leu Thr His Arg Ser Ala Ala Thr
 210 20 25 30
 213 Gln His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu Asn Phe
 214 35 40 45
 217 Thr Ile Ala Glu Ala Leu Tyr His Gln Phe Pro Arg Cys Asn Glu Gly
 218 50 55 60
 221 Glu Leu Ser Arg Met Arg Ala Thr Leu Val Arg Glu Pro Thr Leu Ala
 222 65 70 75 80
 225 Ile Leu Ala Arg Gln Phe Glu Leu Gly Asp Tyr Met Ser Leu Gly Ser
 226 85 90 95
 229 Gly Glu Leu Lys Asn Gly Gly Phe Arg Arg Glu Ser Ile Leu Ala Asp
 230 100 105 110

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233 Cys Val Glu Ala Ile Ile Gly Ala Met Ser Leu Asp Gln Gly Leu Ala
 234 115 120 125
 237 Val Thr Thr Gln Val Ile Arg Asn Trp Tyr Gln Gln Leu Leu Ala Glu
 238 130 135 140
 241 Ile Lys Pro Gly Asp Asn Gln Lys Asp Ala Lys Thr Arg Leu Gln Glu
 242 145 150 155 160
 245 Tyr Leu Gln Gly Lys His Leu Pro Leu Pro Thr Tyr Glu Val Val Asn
 246 165 170 175
 249 Ile Gln Gly Glu Ala His Cys Gln Ile Phe Thr Val Lys Cys Lys Val
 250 180 185 190
 253 Lys Ser Ala Glu Lys Ile Asp Arg Thr Phe Val Ala Lys Gly Ser Ser
 254 195 200 205
 257 Arg Arg Lys Ala Glu Gln Ala Ala Ala Glu Gln Ile Leu Lys Glu Leu
 258 210 215 220
 261 Asp Ile Lys
 262 225
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 267 <212> TYPE: PRT
 268 <213> ORGANISM: unknown
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 271 <223> OTHER INFORMATION: relevant region from S. typhimurium
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 276 1 5 10 15
 279 Phe Asn His Gln Glu Leu Leu Gln Gln Ala Leu Thr His Arg Ser Ala
 280 20 25 30
 283 Ser Ser Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu
 284 35 40 45
 287 Ser Phe Val Ile Ala Asn Ala Leu Ser Arg Phe Pro Arg Val Asp Glu
 288 50 55 60
 291 Gly Asp Met Ser Arg Met Arg Asp Pro Leu Val Arg Gly Asn Thr Leu
 292 65 70 75 80
 295 Ala Glu Leu Ala Arg Glu Phe Asp Leu Gly Glu Cys Leu Arg Leu Gly
 296 85 90 95
 299 Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu Ala
 300 100 105 110
 303 Asp Thr Val Glu Ala Leu Ile Gly Gly Val Phe Leu Asp Ser Asn Ile
 304 115 120 125
 307 Gln Thr Val Glu Gln Leu Ile Leu Asn Trp Tyr Lys Thr Arg Leu Asp
 308 130 135 140
 311 Glu Ile Ser Pro Gly Asp Lys Gln Lys Asp Pro Lys Thr Arg Leu Gln
 312 145 150 155 160
 315 Glu Tyr Leu Gln Gly Arg His Leu Pro Leu Pro Ser Tyr Leu Val Val
 316 165 170 175
 319 Gln Val Arg Gly Glu Ala His Asp Gln Glu Phe Thr Ile His Cys Gln
 320 180 185 190
 323 Val Ser Gly Leu Ser Glu Pro Val Val Gly Thr Gly Ser Ser Arg Arg
 324 195 200 205

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Input Set : A:\NEB-238-PUS.ST25.txt
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 328 210 215 220
 331 <210> SEQ ID NO: 12
 332 <211> LENGTH: 226
 333 <212> TYPE: PRT
 334 <213> ORGANISM: unknown
 336 <220> FEATURE:
 337 <223> OTHER INFORMATION: relevant region from E. coli
 339 <400> SEQUENCE: 12
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 342 1 5 10 15
 345 Phe Asn His Gln Glu Leu Leu Gln Gln Ala Leu Thr His Arg Ser Ala
 346 20 25 30
 349 Ser Ser Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu
 350 35 40 45
 353 Ser Tyr Val Ile Ala Asn Ala Leu Tyr His Arg Phe Pro Arg Val Asp
 354 50 55 60
 357 Glu Gly Asp Met Ser Arg Met Arg Ala Thr Leu Val Arg Gly Asn Thr
 358 65 70 75 80
 361 Leu Ala Glu Leu Ala Arg Glu Phe Glu Leu Gly Glu Cys Leu Arg Leu
 362 85 90 95
 365 Gly Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu
 366 100 105 110
 369 Ala Asp Thr Val Glu Ala Leu Ile Gly Gly Val Phe Leu Asp Ser Asp
 370 115 120 125
 373 Ile Gln Thr Val Glu Lys Leu Ile Leu Asn Trp Tyr Gln Thr Arg Leu
 374 130 135 140
 377 Asp Glu Ile Ser Pro Gly Asp Lys Gln Lys Asp Pro Lys Thr Arg Leu
 378 145 150 155 160
 381 Gln Glu Tyr Leu Gln Gly Arg His Leu Pro Leu Pro Thr Tyr Leu Val
 382 165 170 175
 385 Val Gln Val Arg Gly Glu Ala His Asp Gln Glu Phe Thr Ile His Cys
 386 180 185 190
 389 Gln Val Ser Gly Leu Ser Glu Pro Val Val Gly Thr Gly Ser Ser Arg
 390 195 200 205
 393 Arg Lys Ala Glu Gln Ala Ala Ala Glu Gln Ala Leu Lys Lys Leu Glu
 394 210 215 220
 397 Leu Glu
 398 225
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 403 <212> TYPE: PRT
 404 <213> ORGANISM: unknown
 406 <220> FEATURE:
 407 <223> OTHER INFORMATION: relevant region from V. cholerae
 409 <400> SEQUENCE: 13
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 412 1 5 10 15
 415 Lys Glu Thr Glu Leu Leu Asn Leu Ala Leu Thr His Arg Ser Ala Asn

VERIFICATION SUMMARY DATE: 07/31/2006
PATENT APPLICATION: US/10/586,720 TIME: 14:43:45

Input Set : A:\NEB-238-PUS.ST25.txt
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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date